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<210> 510

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 510

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
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 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
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 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
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 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
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 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
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 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
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 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
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 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
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 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
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 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
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 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
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 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

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 580 585 590
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 740 745 750
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 Gly His His His His His His
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<210> 514

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 514

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
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Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
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 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
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 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
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 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
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 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
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 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
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 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
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 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
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 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
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 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
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 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
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 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
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 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
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 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
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 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
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 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
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 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
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gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg	2460
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<210> 518

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 518

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215						220			
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	

Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	260	265	270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	275	280	285	
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	290	295	300	
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	305	310	315	320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	325	330	335	
Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu	340	345	350	
Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	Leu	355	360	365	
Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	370	375	380	
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	385	390	395	400
Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	Asn	405	410	415	
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	His	420	425	430	
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	435	440	445	
Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Leu	450	455	460	
Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475	480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	485	490	495	
Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys	500	505	510	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525	
Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	530	535	540	
Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
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 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
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 Gly His His His His His His
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<210> 519

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 519
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 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240
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 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
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 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
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gcggcttttg	ccaaggaggc	catggagaag	gcctatcccc	tcgccgtgcc	cctggaggtg	2460
gaggtgggga	tgggggagga	ctggccttcc	gccaaagggtc	accaccacca	ccaccac	2517
<210>	522					
<211>	839					
<212>	PRT					

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 522

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	625	630	635								640	
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp		645	650								655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr		660	665								670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu		675	680								685	
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val		690	695								700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr		705	710								715	720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala		725	730								735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met		740	745								750	
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys		755	760								765	
Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val		770	775								780	
Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val		785	790								795	800
Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val		805	810								815	
Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys		820	825								830	
Gly	His	His	His	His	His	His											835										

<210> 523

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 523

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33

<210> 524
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 524
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gcggctttgg	ccaaggaggc	catggagaag	gcctatcccc	tcgccgtgcc	cctggaggtg	2460
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<210> 526

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 526

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
	290					295					300				
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
305					310					315					320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
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 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
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 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
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 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
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 Gly His His His His His His
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<210> 527

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 527

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39

<210> 528

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 528
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 <210> 529
 <211> 2517
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 <213> Artificial Sequence
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 <223> Synthetic

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 ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccgag gcccctcct tccgccacga ggcctacggg 240
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 aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360
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<210> 530

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 530

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			

Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
50						55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			
Leu	Gly	Gly	Glu	Lys	Pro	Arg	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
	290					295					300				
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
305					310					315					320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala
				325					330					335	
Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu
			340					345					350		
Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	Leu
		355					360					365			
Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser
	370					375					380				

Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	385	390	395	400
Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	Asn	405	410	415	
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	His	420	425	430	
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	435	440	445	
Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Leu	450	455	460	
Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475	480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	485	490	495	
Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys	500	505	510	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525	
Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	530	535	540	
Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val	595	600	605	
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	625	630	635	640
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	645	650	655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685	
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	705	710	715	720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 531

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 531

cacgagttcg gccttctggg aggggagaag ccccgaggagg agggcccttg gcc

54

<210> 532

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 532

gggccagggg gcctcctccc ggggcttctc ccctcccaga aggccgaact cgtg

54

<210> 533

<211> 2517

<212> DNA

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<220>

<223> Synthetic

<400> 533

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<210> 534

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 534

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70				75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Leu	450	455	460	
Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475	480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	485	490	495	
Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys	500	505	510	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525	
Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	530	535	540	
Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val	595	600	605	
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	625	630	635	640
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	645	650	655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685	
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	705	710	715	720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	725	730	735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	740	745	750	
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	755	760	765	
Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	770	775	780	

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830

Gly His His His His His His
 835

<210> 535

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 535
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33

<210> 536

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 536
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33

<210> 537

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag

120

ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg

180

gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg

240

gggtacaagg	cgggccgggc	ccccacgccg	gaggactttc	cccggcaact	cgccctcatc	300
aaggagctgg	tggacctcct	ggggttcacg	cgctcgagg	tcccgggcta	cgaggcggac	360
gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcatactc	420
accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccacccccgag	480
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gcccacctct	ccggggacga	aaacctgatc	agggctcttc	aggaggggaa	ggacatccac	1920
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cgggcggcca	agacggtgaa	cttcggcgctc	ctctacggca	tgtccgcca	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100

ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
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 ctctccagg tcgccaacga gctcctcctg gaggccccc aagcgcgggc cgaggaggtg 2400
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 538

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 538

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	

Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp		
			180					185					190				
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu		
		195					200					205					
Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg		
	210					215					220						
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu		
225					230					235					240		
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu		
				245					250					255			
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala		
			260					265					270				
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu		
	275						280					285					
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu		
	290					295					300						
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala		
305					310					315					320		
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala		
				325					330					335			
Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu		
			340					345					350				
Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	Leu		
		355					360					365					
Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser		
	370					375					380						
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr		
385					390					395					400		
Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	Asn		
				405					410					415			
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	His		
			420					425					430				
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr		
		435					440					445					
Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Leu		
	450					455					460						
Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly		
465					470					475					480		
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe		
				485					490					495			
Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys		
			500					505					510				

Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525
Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	530	535	540
Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	Arg	545	550	555
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val	595	600	605
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	625	630	635
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	645	650	655
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	705	710	715
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	725	730	735
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	740	745	750
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	755	760	765
Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	770	775	780
Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val	785	790	795
Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val	805	810	815
Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	820	825	830
Gly	His	His	His	His	His	His	His	His	His	His	His	His	His	His	His	835		

<210> 539
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 539
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 <210> 540
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 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 540
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 gaggggtacc tcatcacccc ggcttggtt tgggaaaagt acggcctgag gcccgaccag 540
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tacgtggaaa	ccctcttcgg	aagaaggcgc	tacgtgcccc	acctcaacgc	ccgggtgaag	2220
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atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag 2400
 gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gccctggag 2460
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<210> 542

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 542

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val	50	55	60	
Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	65	70	75	80
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	85	90	95	
Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	100	105	110	
Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	115	120	125	
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	130	135	140	
Lys	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	145	150	155	160
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	165	170	175	
Arg	Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	180	185	190	
Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	195	200	205	
Leu	Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	210	215	220	

Arg 225	Leu	Lys	Pro	Ala	Ile 230	Arg	Glu	Lys	Ile	Leu 235	Ala	His	Met	Asp	Asp 240
Leu	Lys	Leu	Ser	Trp 245	Asp	Leu	Ala	Lys	Val 250	Arg	Thr	Asp	Leu	Pro	Leu 255
Glu	Val	Asp	Phe 260	Ala	Lys	Arg	Arg	Glu 265	Pro	Asp	Arg	Glu	Gly 270	Leu	Lys
Ala	Phe	Leu 275	Glu	Arg	Leu	Glu	Phe 280	Gly	Ser	Leu	Leu	His 285	Glu	Phe	Gly
Leu	Leu 290	Gly	Gly	Glu	Lys	Pro 295	Arg	Glu	Glu	Ala	Pro 300	Trp	Pro	Pro	Pro
Glu 305	Gly	Ala	Phe	Val	Gly 310	Phe	Val	Leu	Ser	Arg 315	Lys	Glu	Pro	Met	Trp 320
Ala	Asp	Leu	Leu	Ala 325	Leu	Ala	Ala	Cys	Arg 330	Gly	Gly	Arg	Val	His 335	Arg
Ala	Ala	Asp	Pro 340	Leu	Ala	Gly	Leu	Lys 345	Asp	Leu	Lys	Glu	Val 350	Arg	Gly
Leu	Leu	Ala 355	Lys	Asp	Leu	Ala	Val 360	Leu	Ala	Ser	Arg	Glu 365	Gly	Leu	Asp
Leu	Val 370	Pro	Gly	Asp	Asp	Pro 375	Met	Leu	Leu	Ala	Tyr 380	Leu	Leu	Asp	Pro
Ser 385	Asn	Thr	Thr	Pro	Glu 390	Gly	Val	Ala	Arg	Arg 395	Tyr	Gly	Gly	Glu	Trp 400
Thr	Glu	Asp	Ala	Ala 405	His	Arg	Ala	Leu	Leu 410	Ser	Glu	Arg	Leu	His 415	Arg
Asn	Leu	Leu	Lys 420	Arg	Leu	Glu	Gly	Glu 425	Glu	Lys	Leu	Leu	Trp 430	Leu	Tyr
His	Glu	Val 435	Glu	Lys	Pro	Leu	Ser 440	Arg	Val	Leu	Ala	His 445	Met	Glu	Ala
Thr	Gly 450	Val	Arg	Arg	Asp	Val 455	Ala	Tyr	Leu	Gln	Ala 460	Leu	Ser	Leu	Glu
Leu 465	Ala	Glu	Glu	Ile	Arg 470	Arg	Leu	Glu	Glu	Glu 475	Val	Phe	Arg	Leu	Ala 480
Gly	His	Pro	Phe	Asn 485	Leu	Asn	Ser	Arg	Asp 490	Gln	Leu	Glu	Arg	Val	Leu 495
Phe	Asp	Glu	Leu 500	Arg	Leu	Pro	Ala	Leu 505	Lys	Lys	Thr	Lys	Lys 510	Thr	Gly
Lys	Arg	Ser 515	Thr	Ser	Ala	Ala	Val 520	Leu	Glu	Ala	Leu	Arg 525	Glu	Ala	His
Pro	Ile 530	Val	Glu	Lys	Ile	Leu 535	Gln	His	Arg	Glu	Leu 540	Thr	Lys	Leu	Lys
Asn 545	Thr	Tyr	Val	Asp	Pro 550	Leu	Pro	Ser	Leu	Val 555	His	Pro	Arg	Thr	Gly 560

Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu
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Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu
			580					585					590		
Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu
		595					600					605			
Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu
	610					615					620				
Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile
625					630					635					640
His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val
				645					650					655	
Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu
			660					665					670		
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr
		675					680					685			
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys
	690					695					700				
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly
705					710					715					720
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn
				725					730					735	
Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
			740					745					750		
Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val
		755					760					765			
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
	770					775					780				
Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu
785					790					795					800
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
				805					810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala
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Lys	Gly	His	His	His	His	His	His								
		835					840								

<210> 543

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 543

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gagccggtgc aggcggtcta cggttcgcc aagagcctcc tcaaggccct cagagaggac      180
ggggacgcgg tgatcgtggt ctttgacgcc gaggccccct ctttcgccca cgaggcctac      240
gggggggtaca aggcggggccg ggccccacg ccggaggact ttccccggca actcgccctc      300
atcaaggagc tgggtggacct cctggggttc acgcgcctcg aggtcccggg ctacgaggcg      360
gacgacgtcc tggccaccct ggccaagaag gcggaaggagg agggctacga ggtccgcctc      420
ctcaccgcgg acaaagacct ttaccagctc ctttcgcacc gcatccacgt cctccacccc      480
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<210> 544

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 544

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val
	50					55					60				
Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr
65					70					75				80	
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg
				85					90					95	

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg
 100 105 110
 Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala
 115 120 125
 Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
 130 135 140
 Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
 145 150 155 160
 Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
 165 170 175
 Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
 180 185 190
 Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys
 195 200 205
 Leu Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
 210 215 220
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320
 Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830
 Lys Gly His His His His His His
 835 840

<210> 545

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 545

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50

<210> 546

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 546

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50

<210> 547

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 547

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33

<210> 548
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 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 548
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 <212> DNA
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 <400> 549
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<210> 550

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 550

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			20					25					30			
Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys	
		35					40					45				
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg	
	50					55					60					
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	
65					70					75					80	
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys	
				85					90					95		
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly	
			100					105					110			
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu	
		115					120					125				
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	130					135					140					
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala	
145					150					155					160	
Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu	
				165					170					175		
Leu	Phe	Gly	Ser	Pro	Arg	Leu	Ala	Arg	Asn	Leu	Ala	Ile	Thr	Gly	Lys	
			180					185					190			
Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Asp	Val	Lys	Pro	Glu	Ile	
		195					200					205				
Ile	Ile	Leu	Glu	Ser	Asn	Leu	Lys	Arg	Leu	Gly	Leu	Thr	Arg	Glu	Gln	
	210					215					220					
Leu	Ile	Asp	Ile	Ala	Ile	Leu	Val	Gly	Thr	Asp	Ala	Asn	Glu	Gly	Val	
225					230					235					240	
Lys	Gly	Val	Gly	Val	Lys	Lys	Ala	Leu	Asn	Tyr	Ile	Lys	Thr	Tyr	Gly	
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 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
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 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335

<210> 551

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 551

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33

<210> 552

<211> 1008

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 552

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<211> 336

<212> PRT

<213> Artificial Sequence

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<223> Synthetic

<400> 553

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 Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
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 Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
 85 90 95
 Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
 100 105 110
 Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
 115 120 125
 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
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 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
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 Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
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 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
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 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Arg Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
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 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
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 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
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17

<210> 558

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<212> DNA

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<211> 881

<212> PRT

<213> Artificial Sequence

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<223> Synthetic

<400> 560

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 35 40 45
 Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60
 Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
 85 90 95
 Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
 100 105 110
 Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
 115 120 125
 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
 130 135 140
 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160
 Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
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Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
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 275 280 285
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<223> Synthetic

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aacttcggcg tcctctacgg catgtccgcc cataggtctt cccaggagct tgccatcccc	2160

tacgaggagg cggtggcctt tatagagcgc tacttccaaa gcttcccca ggtgcggggcc 2220
 tggatagaaa agaccctgga ggaggggagg aagcggggct acgtggaaac cctcttcgga 2280
 agaaggcgct acgtgcccga cctcaacgcc cgggtgaaga gcgtcaggga ggccgcggag 2340
 cgcattggcct tcaacatgcc cgtccagggc accgccgccg acctcatgaa gctcgccatg 2400
 gtgaagctct tccccgcct cggggagatg gggggccgca tgctcctcca ggtcgccaac 2460
 gagctcctcc tggaggcccc ccaagcgcg ggcgaggagg tggcggtttt ggccaaggag 2520
 gccatggaga aggcctatcc cctcgccgtg ccctggagg tggaggtggg gatgggggag 2580
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<210> 564

<211> 873

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 564

Met	Gly	Ala	Asp	Ile	Gly	Asp	Leu	Phe	Glu	Arg	Glu	Glu	Val	Glu	Leu
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Glu	Tyr	Phe	Ser	Gly	Lys	Lys	Ile	Ala	Val	Asp	Ala	Phe	Asn	Thr	Leu
			20					25					30		
Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys
		35					40					45			
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg
	50					55					60				
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp
65					70				75						80
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys
				85					90					95	
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly
			100					105					110		
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu
		115					120					125			
Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro
	130					135					140				
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala
145					150					155					160
Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu
				165					170					175	

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Leu Glu Glu Ala Pro Trp Pro Pro
 325 330 335
 Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met
 340 345 350
 Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His
 355 360 365
 Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg
 370 375 380
 Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu
 385 390 395 400
 Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp
 405 410 415
 Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu
 420 425 430
 Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His
 435 440 445
 Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu
 450 455 460
 Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu
 465 470 475 480
 Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu
 485 490 495
 Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu
 500 505 510

Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val
 515 520 525
 Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr
 530 535 540
 Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala
 545 550 555 560
 His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu
 565 570 575
 Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr
 580 585 590
 Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg
 595 600 605
 Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro
 610 615 620
 Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala
 625 630 635 640
 Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His
 645 650 655
 Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp
 660 665 670
 Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala
 675 680 685
 Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val
 690 695 700
 Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro
 705 710 715 720
 Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro
 725 730 735
 Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg
 740 745 750
 Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu
 755 760 765
 Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe
 770 775 780
 Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met
 785 790 795 800
 Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu
 805 810 815
 Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu
 820 825 830
 Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu
 835 840 845

Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser
 850 855 860

Ala Lys Gly His His His His His His
 865 870

<210> 565

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 565

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cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga	180
atcctataca gagtctccaa catggctcgag gtgggaatca ggccggtgtt tgtattcgac	240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggctgag	300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct	360
caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct tttaagttac	420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca	480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc	540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc	600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctggggttg	660
acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgagggtgtg	720
aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg	780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg	840
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc	900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgag	960
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tgggcggagc ttaaagccct ggccgcctgc aggggcggcc gcgtccaccg ggcccccgag	1140
ccttataaag ccctcaggga cctgaaggag gcgcgggggc ttctcgccaa agacctgagc	1200
gttctggccc tgagggaagg ccttggcctc ccgcccggcg acgaccccat gtcctcgcc	1260
tacctcctgg acccttcgaa caccaccccc gaggggggtgg cccggcgcta cggcggggag	1320

tggacggagg aggcggggga gcggggccgc ctttccgaga ggctcttcgc caacctgctt	1380
aagaggcttg agggggagga gaggtcctt tggctttacc gggaggtgga gagggccctt	1440
tccgtgtcc tggcccatat ggaggccacg ggggtgcgc tggacgtggc ctatctcagg	1500
gccttgctcc tggaggtggc cgaggagatc gccgcctcg aggcgaggt cttccgectg	1560
gccggccacc ctttcaacct caactcccgc gaccagctgg aaagggtcct ctttgacgag	1620
ctagggcttc ccgccatcaa gaagacgcaa aagaccggca agcgctccac cagcgccgc	1680
gtcctggagg ccctccgga ggcccacccc atcgtggaga agatcctgca gtaccgggag	1740
ctcaccaagc tgaagagcac ctacattgac cccttgccgc acctcatcca ccccaggacg	1800
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gatcccaacc tccagaacat ccccgctcgc acccgcttg ggcagaggat ccgccgggccc	1920
ttcatcgccg aggaggggtg gctattggtg gccctggact atagccagat agagctcagg	1980
gtgctggccc acctctccgc cgacgagaac ctgatccggg tcttccagga ggggcgggac	2040
atccacacgg agaccgccag ctggatgttc ggcgtccccc gggaggccgt ggacccctg	2100
atgcgccggg cggccaagac catcaacttc ggggtcctct acggcatgtc ggcccaccgc	2160
ctctcccagg agctagccat cccttacgag gaggcccagg ctttcattga gcgctacttt	2220
cagagcttcc ccaaggtgcg ggccctggatt gagaagacct tggaggaggg caggaggcgg	2280
gggtacgtgg agaccctctt cggccgccgc cgctacgtgc cagacctaga ggcccgggtg	2340
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gccgacctca tgaagctggc tatggtgaag ctcttcccca ggctggagga aatgggggcc	2460
aggatgctcc ttcaggtcgc caacgagctg gtccctcagg cccaaaaga gagggcggag	2520
gccgtggccc ggctggccaa ggaggtcatg gagggggtgt atcccctggc cgtgccctg	2580
gaggtggagg tggggatagg ggaggactgg ctctccgcca aggagcacca ccaccaccac	2640
cac	2643

<210> 566

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 566

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Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
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Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35 40 45
Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50 55 60
Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65 70 75 80
Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
85 90 95
Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
100 105 110
Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
115 120 125
Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
130 135 140
Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145 150 155 160
Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
165 170 175
Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
180 185 190
Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
195 200 205
Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
210 215 220
Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
225 230 235 240
Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
245 250 255
Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
260 265 270
Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
275 280 285
Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
290 295 300
Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
305 310 315 320

Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335
 Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
 340 345 350
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
 355 360 365
 Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
 370 375 380
 Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
 385 390 395 400
 Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
 405 410 415
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 420 425 430
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
 435 440 445
 Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Leu Lys Arg Leu Glu
 450 455 460
 Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
 465 470 475 480
 Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
 485 490 495
 Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
 500 505 510
 Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 515 520 525
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
 530 535 540
 Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 545 550 555 560
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 565 570 575
 Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
 580 585 590
 Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 595 600 605
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 610 615 620
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 625 630 635 640
 Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
 645 650 655

Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	660	665	670	
Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Glu	Thr	Ala	Ser	Trp	675	680	685	
Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	690	695	700	
Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	705	710	715	720
Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Gln	Ala	Phe	Ile	725	730	735	
Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	740	745	750	
Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	755	760	765	
Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg	Val	Lys	Ser	Val	Arg	770	775	780	
Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	785	790	795	800
Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Glu	805	810	815	
Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala	Asn	Glu	Leu	Val	Leu	820	825	830	
Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala	Arg	Leu	Ala	Lys	Glu	835	840	845	
Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	850	855	860	
Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu	His	His	His	His	His	865	870	875	880
His																			

<210> 567

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 567

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cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga	180
atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtgtt tgtattcgac	240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag	300
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caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct ttttaagttac	420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca	480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc	540
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tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctggggttg	660
acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgagggtgtg	720
aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg	780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg	840
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tgggcggagc ttaaagccct ggccgcctgc aggggcggcc gcgtccaccg ggcccccgag	1140
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ctaccaagc tgaagagcac ctacattgac cccttgccgg acctcatcca ccccaggacg	1800
ggccgcctcc acaccgctt caaccagacg gccacggcca cgggcaggct aagtagctcc	1860

gatcccaacc tccagaacat ccccgctccgc accccgcttg ggcagaggat ccgcccgggcc 1920
 ttcacgcgcg aggaggggtg gctattggtg gccctggact atagccagat agagctcagg 1980
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 gccgacctca tgaagctggc tatggtgaag ctcttcccca ggctggagga aatggggggc 2460
 aggatgctcc ttcaggtcca caacgagctg gtccctcgagg ccccaaaga gaggcgagg 2520
 gccgtggccc ggctggccaa ggaggtcatg gagggggtgt atcccctggc cgtgcccctg 2580
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<210> 568

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 568

Met	Gly	Ala	Asp	Ile	Gly	Asp	Leu	Phe	Glu	Arg	Glu	Glu	Val	Glu	Leu
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Glu	Tyr	Phe	Ser	Gly	Lys	Lys	Ile	Ala	Val	Asp	Ala	Phe	Asn	Thr	Leu
			20					25					30		
Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys
		35					40					45			
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg
	50					55					60				
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp
65					70				75					80	
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys
				85					90					95	
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly
			100					105					110		

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
 115 120 125
 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
 130 135 140
 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160
 Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
 165 170 175
 Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335
 Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
 340 345 350
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
 355 360 365
 Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
 370 375 380
 Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
 385 390 395 400
 Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
 405 410 415
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 420 425 430
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
 435 440 445

Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu
 450 455 460
 Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
 465 470 475 480
 Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
 485 490 495
 Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
 500 505 510
 Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 515 520 525
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
 530 535 540
 Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 545 550 555 560
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 565 570 575
 Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
 580 585 590
 Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 595 600 605
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 610 615 620
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 625 630 635 640
 Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
 645 650 655
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 660 665 670
 Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp
 675 680 685
 Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 690 695 700
 Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 705 710 715 720
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile
 725 730 735
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 740 745 750
 Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly
 755 760 765
 Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg
 770 775 780

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 785 790 795 800
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu
 805 810 815
 Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asn Glu Leu Val Leu
 820 825 830
 Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu
 835 840 845
 Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
 850 855 860
 Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu His His His His His
 865 870 875 880
 His

<210> 569

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 569

gagcggataa caatttcaca cagg

24

<210> 570

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 570

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30

<210> 571

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 571

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caggcgggtgt acgggttttg caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tgtttgacgc caaggccccc tccttcgcc accagacctt cgaggcctac	240
aaggcggggc gggctccac ccccgaggac tttcccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggctt ggagcgctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaagag gagggctacg aggtccgcct cctcaccgcc	420
gacaaagacc tttaccagct cctttccgac cgcattccacg tcctccaccc cgaggggtac	480
ctcatcacc cggcctggct ttgggaaaag tacggcctga ggcccgacca gtgggcccac	540
taccgggccc tgaccgggga cgagtccgac aaccttccc ggggtcaagg catcggggag	600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg	660
gaccggctga agcccccat cggggagaag atcctggccc acatggacga tctgaagctc	720
tcctgggacc tggccaaggt ggcaccgac ctgcccctgg aggtggactt cgccaaaagg	780
cgggagccc accgggagg ggagaagccc cgggaggagg cccctggcc cccgcccga	840
ggggccttcg tgggcttctt cctttcccgc cccgagccca tgtgggcgga gcttaaagcc	900
ctggccgcct gcaggggcgg ccgcgtgcac cgggcagcag accccttggc ggggctaaag	960
gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgaggag	1020
gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctcct ggaccttcg	1080
aacaccaccc ccgaggggggt ggcgcggcgc tacggggggg agtggacgga ggacgccgcc	1140
caccgggccc tcctctcgga gaggtccat cggaacctcc ttaagcgctt cgagggggag	1200
gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctcccgggt cctggcccat	1260
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gcggaggaga tccgccgcct cgaggaggag gtcttcgcgt tggcgggcca ccccttcaac	1380
ctcaactccc gggaccagct ggaaagggtg ctctttgacg agcttaggct tccgccttg	1440
aagaagacga agaagacagg caagcgctcc accagcgccg cgggtgctgga ggccctacgg	1500
gaggcccacc ccatcgtgga gaagatctc cagcaccggg agctcaccaa gctcaagaac	1560
acctacgtgg accccctccc aagcctcgtc caccgagga cgggcgcctt ccacaccgc	1620
ttcaaccaga cggccacggc cacggggagg cttagtagct ccgaccccaa cctgcagaac	1680
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ggggacgaaa acctgatcag ggtcttccag gaggggaagg acatccacac ccagaccgca	1860

agctggatgt tcggcgctccc cccggaggcc gtggaccccc tgatgcgccg ggcggccaag 1920
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 atccccctacg aggaggcggg ggcctttata gagcgctact tccaaagctt cccaagggtg 2040
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 ttcggaagaa ggcgctacgt gcccgcctc aacgcccggg tgaagagcgt caggaggaggcc 2160
 gcgagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc 2220
 gccatggtga agctcttccc ccgcctccgg gagatggggg ccgcatgct cctccaggtc 2280
 gccaacgagc tcctcctgga ggccccccaa gcgcggggccg aggaggtggc ggctttggcc 2340
 aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtggggatg 2400
 ggggaggact ggctttccgc caagggtcac caccaccacc accac 2445

<210> 572

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 572

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
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Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	Leu
	130						135				140				

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
145 150 155 160
Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
165 170 175
Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
180 185 190
Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
195 200 205
Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
210 215 220
Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
225 230 235 240
Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
245 250 255
Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
260 265 270
Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
275 280 285
Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
290 295 300
Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
305 310 315 320
Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
325 330 335
Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
340 345 350
Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
355 360 365
Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
370 375 380
Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
385 390 395 400
Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
405 410 415
Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
420 425 430
Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
435 440 445
Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
450 455 460
Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
465 470 475 480

Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 725 730 735
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
 740 745 750
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
 755 760 765
 Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
 770 775 780
 Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
 785 790 795 800
 Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
 805 810 815

<210> 573
 <211> 2520
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 573
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 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac 180
 ggggacgcgg tgatcgtggt ctttgacgcc aaggccccct ccttcgccca cgaggcctac 240
 ggggggtaca aggcggggccg ggccccacc ccggaggact tccccgccca gctcgccttg 300
 gtcaagcggc tgggtggacct tctgggcctg gtccgcctcg agggcccggt gtacgaggcg 360
 gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcac 420
 ctcaccgccg accgcgacct ctaccaactc gtctccgacc gcatccacgt cctccacccc 480
 gaggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag 540
 tgggtggact accgggcctt ggccggggac ccttcgcaca acatcccccg cgtgaagggc 600
 atcggggaga agacggcggc caagctgac cgggagtggg gaagcctgga aaacctcctc 660
 aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat 720
 ctgaagctct cctgggacct ggccaagggt cgcaccgacc tgcccctgga ggtggacttc 780
 gccaaaaggc gggagcccga ccgggagagg cttagggcct ttctggagag gcttgagttt 840
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 tggccccgc cgggaagggc cttcgtgggc ttcgtcctct cccgccccga gcccatgtgg 960
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 ctttccctgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg 1440
 ggccacccct tcaacctcaa ctcccgggac cagctggaaa gggtgctctt tgacgagctt 1500

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aggcttcccg ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg 1560
ctggaggccc tacgggagge ccaccccatc gtggagaaga tcctccagca ccgggagctc 1620
accaagctca agaacaccta cgtggacccc ctcccaagcc tcgtccaccc gaggaacgggc 1680
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gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gccctggag 2460
gtggaggtgg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac 2520

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<210> 574

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 574

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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20          25          30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35          40          45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val
50          55          60
Ile Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr
65          70          75          80

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Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
 85 90 95
 Gln Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg
 100 105 110
 Leu Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala
 115 120 125
 Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
 130 135 140
 Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Ile His Val Leu His Pro
 145 150 155 160
 Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu
 165 170 175
 Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser
 180 185 190
 Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys
 195 200 205
 Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp
 210 215 220
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
 305 310 315 320
 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415

Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	420	425	430	
His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	435	440	445	
Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	450	455	460	
Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	465	470	475	480
Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	485	490	495	
Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	500	505	510	
Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	515	520	525	
Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	530	535	540	
Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	545	550	555	560
Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	565	570	575	
Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	580	585	590	
Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	595	600	605	
Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	610	615	620	
Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	625	630	635	640
His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	645	650	655	
Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	660	665	670	
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	675	680	685	
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	690	695	700	
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	705	710	715	720
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	725	730	735	
Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	740	745	750	

Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val
		755					760					765			
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
	770					775					780				
Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu
785					790					795					800
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
			805						810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala
		820						825					830		
Lys	Gly	His	His	His	His	His	His								
		835					840								

<210> 575

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 575

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caggcgggtgt	acgggtttgc	caagagcctt	ttgaaggcgc	taagggaaga	cggggatgtg	180
gtgatcgtgg	tgtttgacgc	caaggccccc	tccttcgcgc	accagacctt	cgaggcctac	240
aaggcggggc	gggctccccc	ccccgaggac	tttccccggc	agcttgccct	tatcaaggag	300
atggtggacc	ttttgggctt	taccgccttc	gaggtgcccg	gctttgaagc	ggatgacgtc	360
ctggctaccc	tggccaagaa	ggcggaaaag	gaggggtacg	aggtccgcat	cctcaccgcc	420
gacaaagacc	tttaccagct	cctttccgac	cgcattccacg	tcctccaccc	cgaggggtac	480
ctcatcacc	cggcctggct	ttgggaaaag	tacggcctga	ggcccgacca	gtgggccgac	540
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aagacggcga	ggaagcttct	ggaggagtgg	gggagcctgg	aagccctcct	caagaacctg	660
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tcctgggacc	tggccaaggt	gcgcaccgac	ctgcccctgg	aggtggactt	cgccaaaagg	780
cgggagcccc	accgggaggg	ggagaagccc	cgggaggagg	ccccctggcc	cccgcccga	840
ggggccttcg	tgggcttcct	cctttccgc	cccagacca	tgtgggcgga	gcttaaagcc	900
ctggccgcct	gcaggggcgg	ccgcgtgcac	cgggcagcag	accccttggc	ggggctaaag	960

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gggctagacc tcgtgcccgg ggacgacccc atgtctcctcg cctacctcct ggacccttcg	1080
aacaccaccc ccgaggggggt ggcgcggcgc tacggggggg agtggacgga ggacgccgcc	1140
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ctcaactccc gggaccagct ggaaaggggt ctctttgacg agcttaggct tccgccttg	1440
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gagggccacc ccatacgtgga gaagatcctc cagcaccggg agctcaccaa gctcaagaac	1560
acctacgtgg accccctccc aagcctcgtc caccgagga cgggccgcct ccacaccgc	1620
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ggggacgaaa acctgatcag ggtcttccag gaggggaagg acatccacac ccagaccgca	1860
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gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc	2220
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gccaacgagc tcctcctgga ggccccccaa gcgcggggcc aggaggtggc ggctttggcc	2340
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<210> 576

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 576

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
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			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120						125		
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	Leu
	130					135					140				
Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	Tyr
145					150					155					160
Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Asp
				165					170					175	
Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	Leu
			180					185					190		
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu
		195					200					205			
Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys
	210					215					220				
Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	Leu
225					230					235					240
Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp
				245					250					255	
Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Glu	Lys	Pro	Arg	Glu
			260					265					270		
Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Leu	Leu
		275					280					285			
Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys
	290					295					300				
Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys
305					310					315					320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350
 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
 420 425 430
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 725 730 735
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
 740 745 750
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
 755 760 765
 Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
 770 775 780
 Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
 785 790 795 800
 Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
 805 810 815

<210> 577

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 577

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac	180
ggggacgcgg tgatcgtggt ctttgacgcc aaggccccct ccttccgcca cgaggcctac	240
gggggggtaca aggcggggccg ggccccacc ccggaggact tccccgcca gtcgccttg	300
gtcaagcggc tgggtggacct tctgggcttt acccgctcg agggcccggt gtacgaggcg	360
gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcac	420
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gaggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag	540
tgggtggact accgggcctt ggccggggac ccttccgaca acatcccccg cgtgaagggc	600

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gacctcatga agctcgccat ggtgaagctc ttccccgcc tccgggagat gggggccgc	2340

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<210> 578

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 578

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
	35						40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val
	50					55					60				
Ile	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr
65				70						75				80	
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg
			85						90					95	
Gln	Leu	Ala	Leu	Val	Lys	Arg	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg
			100					105					110		
Leu	Glu	Ala	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Gly	Thr	Leu	Ala
	115						120					125			
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp
	130					135					140				
Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro
145					150					155					160
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu
			165					170						175	
Lys	Pro	Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser
			180					185					190		
Asp	Asn	Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys
	195						200					205			
Leu	Ile	Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp
	210					215					220				

Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	225	230	235	240
Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	245	250	255	
Glu	Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	260	265	270	
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	275	280	285	
Leu	Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	290	295	300	
Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	305	310	315	320
Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val	His	Arg	325	330	335	
Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly	340	345	350	
Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	355	360	365	
Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	370	375	380	
Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	385	390	395	400
Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	405	410	415	
Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	420	425	430	
His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	435	440	445	
Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	450	455	460	
Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	465	470	475	480
Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	485	490	495	
Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	500	505	510	
Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	515	520	525	
Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	530	535	540	
Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	545	550	555	560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830
 Lys Gly His His His His His His
 835 840

<210> 579

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 579

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caggcgggtg	acgggtttgc	caagagcctt	ttgaaggcgc	taagggaaga	cggggatgtg	180
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aaggcggggc	gggctccac	ccccgaggac	tttccccggc	agcttgcctt	tatcaaggag	300
atggtggacc	ttttgggcct	ggagcgcctc	gaggtgccgg	gctttgaagc	ggatgacgtc	360
ctggctaccc	tggccaagaa	ggcggaaaag	gagggctacg	aggtccgcct	cctcaccgcc	420
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caccggggcc	tcctctcgga	gaggctccat	cggaacctcc	ttaagcgctt	cgagggggag	1200
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<210> 580

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 580

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
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Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105						110	

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
 130 135 140
 Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
 165 170 175
 Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
 180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
 195 200 205
 Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
 210 215 220
 Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
 225 230 235 240
 Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
 260 265 270
 Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
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 Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
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 Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
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 Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
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 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
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 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365
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 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
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Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
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 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
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 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
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 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
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 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 725 730 735
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
 740 745 750
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Glu Ala
 755 760 765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
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Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
805 810 815

<210> 581

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 581

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caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg      180
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<210> 582

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 582

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			20					25					30		

Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys		
		35					40					45					
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val		
	50					55					60						
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr		
65					70					75					80		
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala		
				85					90					95			
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	Glu	Val		
			100					105					110				
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala		
		115					120					125					
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	Leu		
	130					135					140						
Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	Tyr		
145				150						155					160		
Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Asp		
				165					170					175			
Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	Leu		
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Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu		
		195					200					205					
Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys		
	210					215					220						
Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	Leu		
225					230					235					240		
Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp		
				245					250					255			
Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Glu	Lys	Pro	Arg	Glu		
			260					265					270				
Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Leu	Leu		
		275					280					285					
Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys		
	290					295					300						
Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys		
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Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu		
				325					330					335			
Ala	Ser	Arg	Glu	Gly	Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu		
			340					345					350				
Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala		
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 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480
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 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
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 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
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 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
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 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700

Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 725 730 735
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
 740 745 750
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Glu Ala
 755 760 765
 Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
 770 775 780
 Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
 785 790 795 800
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 805 810 815

<210> 583

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 583

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<210> 584

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 584

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	
			20					25					30			
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	
		35					40					45				
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val	
	50					55					60					
Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	
65					70					75					80	
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	
				85					90					95		
Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	
			100					105					110			
Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	
		115					120					125				
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	
	130					135					140					
Lys	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	
145					150					155					160	
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	
				165					170					175		
Arg	Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	
			180					185					190			
Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	
		195					200					205				
Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	
		210				215						220				
Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	
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Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	
				245					250					255		

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
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 Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
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 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
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 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
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 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
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 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
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 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
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 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
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 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
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 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
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 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
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 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
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 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
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 Lys Gly His His His His His His
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<210> 585

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 585
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gtggtcgtgg tctttgacgc caaggccccc tcttccgcc acgaggccta cgaggcctac 240
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<210> 586

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 586

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			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Gly	Asp	Arg	Asp	Leu
	130					135					140				

Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Arg	Pro	Glu	Gln	Trp	Val	Asp	
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Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile	Pro	Gly	Val	Lys	
				165					170					175		
Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu	Glu	Trp	Gly	Ser	
			180					185					190			
Val	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys	Pro	Ala	Ile	Arg	
		195					200					205				
Glu	Lys	Ile	Leu	Ala	His	Met	Glu	Asp	Leu	Lys	Leu	Ser	Leu	Glu	Leu	
	210					215					220					
Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	
225					230					235					240	
Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	Phe	Leu	Glu	Arg	Leu	Glu	
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Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	Glu	Ser	Pro	Val	Ala	
			260					265					270			
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Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	Asn	Ala	Leu	Ala	
	290					295					300					
Ala	Ala	Trp	Gly	Gly	Arg	Val	His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	
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Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	
				325					330					335		
Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	
			340					345					350			
Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	
	355						360					365				
Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	
	370					375					380					
Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	
385					390					395					400	
Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	
				405					410					415		
Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	
			420					425					430			
Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	
		435					440					445				
Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	
	450					455					460					
Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	
465					470					475					480	

Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 485 490 495
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 500 505 510
 Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu
 515 520 525
 Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 530 535 540
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 545 550 555 560
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 565 570 575
 Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln
 580 585 590
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 595 600 605
 Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp
 610 615 620
 Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 625 630 635 640
 Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 645 650 655
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile
 660 665 670
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 675 680 685
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly
 690 695 700
 Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg
 705 710 715 720
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 725 730 735
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
 740 745 750
 Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu
 755 760 765
 Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu
 770 775 780
 Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
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 Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
 805 810

<210> 587

<211> 2433

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 587

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aaggcggggc gggcccccgc ccccgaggac tcccccggc agctcgccct catcaaggag      300
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ttcaacctca actcccggga ccagctggaa agggtgctct ttgacgagct taggcttccc     1440
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caggtcgcca acgagctcct cctggaggcc cccaagcgc gggccgagga ggtggcggct 2340
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<210> 588

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 588

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Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
          35          40          45
Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
          50          55          60
Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr
65          70          75          80

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Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
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Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
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Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Gly	Asp	Arg	Asp	Leu
	130					135					140				
Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Arg	Pro	Glu	Gln	Trp	Val	Asp
145				150						155					160
Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile	Pro	Gly	Val	Lys
				165					170					175	
Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu	Glu	Trp	Gly	Ser
			180					185					190		
Val	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys	Pro	Ala	Ile	Arg
		195					200					205			
Glu	Lys	Ile	Leu	Ala	His	Met	Glu	Asp	Leu	Lys	Leu	Ser	Leu	Glu	Leu
	210					215					220				
Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly
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Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	Phe	Leu	Glu	Arg	Leu	Glu
				245					250					255	
Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	Glu	Ser	Pro	Val	Ala
			260					265					270		
Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Tyr
		275					280					285			
Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	Asn	Ala	Leu	Ala
	290					295					300				
Ala	Ala	Trp	Gly	Gly	Arg	Val	His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly
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Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala
				325					330					335	
Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro
			340					345					350		
Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly
	355						360					365			
Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg
	370					375					380				
Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu
385				390						395					400
Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu
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 Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg
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 Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 450 455 460
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro
 465 470 475 480
 Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 485 490 495
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 500 505 510
 Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu
 515 520 525
 Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 530 535 540
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 545 550 555 560
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 565 570 575
 Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln
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 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
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Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
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 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
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 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
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 Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe
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 gccaaaggtgc tggaggcg 18
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<210> 801
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 <223> Synthetic
 <400> 801
 caatctcggg ctgcaaagca gac 23
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 <400> 802
 ccaacctgct gagaggcg 18
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 <223> Synthetic
 <400> 806
 ccgccgagat cactctcctc attgaatcc 29
 <210> 807
 <211> 34
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 <223> Synthetic
 <400> 807
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 <210> 808
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 aggattcaat gaggaagagt gatct 25
 <210> 809
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 <211> 24
 <212> DNA
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 ccgtcacgcc tcctcctcat tgaa 24

<210> 812
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 <223> Synthetic
 <400> 812
 ccagtgatga ttttcaccag gcaagta 27
 <210> 813
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 813
 tccagattgg aagcatccat ct 22
 <210> 814
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 814
 ttcaatgagg aggaggc 17
 <210> 815
 <211> 28
 <212> DNA
 <213> Artificial Sequence
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 <400> 815
 cggaagaagc agttggaggc gtgacggt 28

<210> 816
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 <222> (4)..(4)
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 <400> 817
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 <211> 27
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 818
 ccagtgatga ttttcaccag gcaagta 27
 <210> 819
 <211> 23
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<213> Artificial Sequence
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 <400> 819
 atccagattg gaagcatcca tct 23
 <210> 820
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 820
 ttcaatgagg aggaggc 17
 <210> 821
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 821
 cggaagaagc agttggaggc gtgacggt 28
 <210> 822
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 822
 caacgcttcc tccg 14

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<212>	DNA	
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<220>		
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<400>	823	
	ccgtcacgcc tcctcctcat tgaatg	26
<210>	824	
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	ccgtcacgcc tcctcctcat tgaata	26
<210>	825	
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	ccgtcacgcc tcctcctcat tgaatt	26
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	ccaaaagtcc agtgatgatt ttcaccaggc aagta	35

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 <400> 828
 gattcaatga ggaggaggc 19
 <210> 829
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 ccaggaagca agtggaggcg tgacggu 27
 <210> 830
 <211> 13
 <212> DNA
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 <223> Synthetic
 <220>

<221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group. .
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 <211> 26
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 831
 ccgtcacgcc tccttcggag ttggt 26
 <210> 832
 <211> 27
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 832
 ccgtcacgcc tccttcggag ttgggt 27
 <210> 833
 <211> 25
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 833
 gggttgtgga gtgagtgttc aagta 25
 <210> 834
 <211> 24
 <212> DNA

<213> Artificial Sequence
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 <223> Synthetic
 <400> 834
 aaccctaaact ccgaaggcgg cgtg 24
 <210> 835
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 835
 cggaagaagc agttggaggc gtgacggt 28
 <210> 836
 <211> 14
 <212> DNA
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
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 caacgcttcc tccg 14
 <210> 837
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 837
 gccgtcacgc ctctttgggt ttgcttgctc 29

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	gccggtcacgc ctctttgggt ttgottgt	28
<210>	839	
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	tggagtgagt gttcaagtct tcggaga	27
<210>	840	
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	gacaagcaaa cccaaagagg cg	22
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<400>	841	
	cggaagaagc agttggaggc gtgacggc	28

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 <211> 14
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 <223> Synthetic
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 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
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 <210> 843
 <211> 27
 <212> DNA
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 <223> Synthetic
 <400> 843
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 <210> 844
 <211> 26
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 844
 cctgtctcgc tgccttcgga gtttgg 26
 <210> 845
 <211> 25
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<213> Artificial Sequence
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 <223> Synthetic
 <400> 845
 gggttgtgga gtgagtgttc aagta 25
 <210> 846
 <211> 20
 <212> DNA
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 cggaggaagc agttggcagc gagacagg 28
 <210> 848
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 <222> (26)..(26)
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 <400> 848
 cggaggaagc agttggcagc gagacagg 28

<210> 849
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 <213> Artificial Sequence
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 <223> Synthetic
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 <221> modified_base
 <222> (22)..(22)
 <223> The modified nucleotide at this position is amino-deoxy adenosine

 <400> 849
 cggaggaagc agttggcagc gagacagg 28
 <210> 850
 <211> 28
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
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 <222> (18)..(18)
 <223> The modified nucleotide at this position is amino-deoxy adenosine

 <400> 850
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 <210> 851
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 <223> Synthetic

<220>
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 <222> (22)..(22)
 <223> The modified nucleotide at this position is amino-deoxy adenosine

 <220>
 <221> modified_base
 <222> (26)..(26)
 <223> The modified nucleotide at this position is amino-deoxy adenosine

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 cggaggaagc agttggcagc gagacagg 28
 <210> 852
 <211> 28
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 <213> Artificial Sequence
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 <223> Synthetic
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 <221> modified_base
 <222> (18)..(18)
 <223> The modified nucleotide at this position is amino-deoxy adenosine

 <220>
 <221> modified_base
 <222> (26)..(26)
 <223> The modified nucleotide at this position is amino-deoxy adenosine

 <400> 852
 cggaggaagc agttggcagc gagacagg 28
 <210> 853
 <211> 28
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 <222> (18)..(18)
 <223> The modified nucleotide at this position is amino-deoxy adenosine
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 <222> (22)..(22)
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 cggaggaagc agttggcagc gagacagg 28
 <210> 854
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 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 854
 caacgcttcc tccg 14
 <210> 855
 <211> 28
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic

<400> 855 gccgtcacgc ctctgggaca cttgctgc	28
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 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
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 <211> 26
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 860
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 <223> Synthetic
 <400> 861
 gggttgtgga gtgagtgttc aagta 25
 <210> 862
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 862
 gggaaactcc gaaggaggcg 20
 <210> 863
 <211> 27
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 863
 ccaggaagca agtggaggcg tgacggu 27
 <210> 864
 <211> 13
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
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 <210> 865
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 865
 cgccgagatc accttcggag tttggg 26
 <210> 866
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 866
 gggttgtgga gtgagtgttc aagta 25

<210> 867
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 867
 cccaaactcc gaaggtgatc 20
 <210> 868
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 868
 cggaagaagc agttggtgat ctcggcgg 28
 <210> 869
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 869
 caacgcttcc tccg 14
 <210> 870
 <211> 26
 <212> DNA

<213> Artificial Sequence
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 <223> Synthetic
 <400> 870
 aacgaggcgc accttcggag tttggg 26
 <210> 871
 <211> 25
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 <223> Synthetic
 <400> 871
 gggttgtgga gtgagtgttc aagta 25
 <210> 872
 <211> 19
 <212> DNA
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 <220>
 <223> Synthetic
 <400> 872
 cccaaactcc gaaggtgcg 19
 <210> 873
 <211> 29
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 873
 cggaagaagc agttggtgcg cctcgttaa 29
 <210> 874
 <211> 14
 <212> DNA

<213> Artificial Sequence
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 <223> Synthetic
 <220>
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 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 874
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 <210> 875
 <211> 25
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 875
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 <210> 876
 <211> 25
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 876
 gggttgtgga gtgagtgttc aagta 25
 <210> 877
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 877
 gtttgcttgt ccaggtgg 18

<210> 878
 <211> 19
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 878
 ccaaactccg aaggaggcg 19
 <210> 879
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 879
 cggaagaagc agttggaggc gtgacggt 28
 <210> 880
 <211> 14
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
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 <210> 881
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 881

ccgtcacgcc tccttcggag ttg

24

<210> 882

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 882

gggttggtgga gtgagtgttc aagta

25

<210> 883

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 883

gttttgcttg tccaggtgg

19

<210> 884

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 884

ccaaactccg aaggaggcg

19

<210> 885

<211> 28

<212> DNA

<213> Artificial Sequence
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 <223> Synthetic
 <400> 885
 cggaagaagc agttggaggc gtgacggt 28
 <210> 886
 <211> 14
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 <222> (4)..(4)
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 <210> 888
 <211> 25
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 888
 gggttgtgga gtgagtgttc aagta 25

<210> 889
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 gggtttgctt gtccaggtg 19
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 890
 ccaaactccg aaggaggcg 19
 <210> 891
 <211> 28
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 cggaagaagc agttggaggc gtgacggt 28
 <210> 892
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 <400> 893
 ccgtcacgcc tccggagttt ggg 23
 <210> 894
 <211> 26
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 gttgtggagt gagtgttcaa gtatta 26
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 <213> Artificial Sequence
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 tttgcttgtc caggtggtcc ag 22

<210> 896
 <211> 17
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 896
 cccaaactcc ggaggcg 17
 <210> 897
 <211> 28
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 cggaagaagc agttggaggc gtgacggt 28
 <210> 898
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 <222> (4)..(4)
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 dye
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 <210> 899
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 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 899
 cgccgagatc accggagttt ggg 23
 <210> 900
 <211> 26
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 900
 gttgtggagt gagtgttcaa gtatta 26
 <210> 901
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 901
 ttgcttgtc caggtggtcc ag 22
 <210> 902
 <211> 17
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 <400> 902
 ctagtggcct caaaccc 17
 <210> 903
 <211> 28
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<213> Artificial Sequence
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 <400> 903
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 <210> 904
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 <210> 905
 <211> 30
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 905
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 <210> 906
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 906
 cgccgagatc acctttacat tttctatcgt 30

<210> 907
 <211> 24
 <212> DNA
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 <223> Synthetic
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 ccttccttat cctggatctt ggca 24
 <210> 908
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 908
 acgatagaaa atgtaaaggt gatc 24
 <210> 909
 <211> 29
 <212> DNA
 <213> Artificial Sequence
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 <400> 909
 cgcagtgaga atgaggatgat ctcggcggc 29
 <210> 910
 <211> 14
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<220>

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<222> (3)..(3)

<223> The residue at this position is linked to a Z21 quenching group.

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<210> 911

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 911
gtttcttttg tgtctccgca ctgcc 25

<210> 912

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 912
ccagcagtaa atgctccagt tgtaga 26

<210> 913

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 913
tagaacttga agtaggtgc 19

<210> 914

<211> 19

<212> DNA

<213> Artificial Sequence
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 <223> Synthetic
 <400> 914
 caaagaaaac acaggaggc 19
 <210> 915
 <211> 27
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 915
 ccaggaagca agtggaggcg tgacggu 27
 <210> 916
 <211> 13
 <212> DNA
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 <220>
 <223> Synthetic
 <220>
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 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
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 <210> 917
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 917
 aacgaggcgc acctgtgttt tctttg 26

<210> 918
 <211> 26
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 918
 ccagcagtaa atgctccagt tgtaga 26
 <210> 919
 <211> 19
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 919
 tagaacttga agtaggtgc 19
 <210> 920
 <211> 19
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 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 920
 caaagaaaac acaggtgcg 19
 <210> 921
 <211> 27
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 921
 ccaggaagca agtggtgcgc ctcgttt 27

<210> 922
 <211> 13
 <212> DNA
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 <223> Synthetic
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 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
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 <210> 923
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 923
 ccgtcacgcc tcctccagtt gtag 24
 <210> 924
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 924
 aaaatcatct gttaaaccag cagtaaatga 30
 <210> 925
 <211> 20
 <212> DNA

<213> Artificial Sequence
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 <223> Synthetic
 <400> 925
 ctgtgttttc tttgtagaac 20
 <210> 926
 <211> 17
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 926
 ctacaactgg aggaggc 17
 <210> 927
 <211> 27
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 927
 ccaggaagca agtggaggcg tgacggu 27
 <210> 928
 <211> 13
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 <223> Synthetic
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 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
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<210> 929
 <211> 24
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 929
 aacgaggcgc acctccagtt gtag 24
 <210> 930
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 930
 aaaatcatct gttaaaccag cagtaaata 30
 <210> 931
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 931
 ctgtgttttc tttgtagaac 20
 <210> 932
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 932
 ctacaactgg aggtgcg 17

<210> 933
 <211> 27
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 933
 ccaggaagca agtggtgcgc ctcgttt 27
 <210> 934
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 <223> Synthetic
 <220>
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 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
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 <210> 935
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 935
 ccgtcacgcc tcctgtgttt tctttgta 28
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 <211> 32
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<213> Artificial Sequence

<220>

<223> Synthetic

<400> 936

gtaaatccag cagtaaatgc tccagttgta ga

32

<210> 937

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 937

gaacttgaag taggtgcact gtt

23

<210> 938

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 938

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23

<210> 939

<211> 27

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<223> Synthetic

<400> 939

ccaggaagca agtggaggcg tgacggu

27

<210> 940

<211> 13

<212> DNA

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 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
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 <210> 941
 <211> 28
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 <223> Synthetic
 <400> 941
 aacgaggcgc acctgtgttt tctttgta 28
 <210> 942
 <211> 32
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 942
 gtaaatccag cagtaaatgc tccagttgta ga 32
 <210> 943
 <211> 23
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 943
 gaacttgaag taggtgcact gtt 23

<210> 944
 <211> 21
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 944
 tacaaagaaa acacaggtgc g 21
 <210> 945
 <211> 27
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 <213> Artificial Sequence
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 <223> Synthetic
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 ccaggaagca agtggtgcgc ctcgttt 27
 <210> 946
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 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
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 cactgcttcg tgg 13
 <210> 947
 <211> 24
 <212> DNA

<213> Artificial Sequence
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 <223> Synthetic
 <400> 947
 ccgtcacgcc tcctccagtt gtaa 24
 <210> 948
 <211> 24
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 948
 ccgtcacgcc tcctccagtt gtat 24
 <210> 949
 <211> 24
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 949
 ccgtcacgcc tcctccagtt gtac 24
 <210> 950
 <211> 30
 <212> DNA
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 <223> Synthetic
 <400> 950
 aaaatcatct gtaaattccag cagtaaatga 30
 <210> 951
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<213> Artificial Sequence
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 <223> Synthetic
 <400> 951
 ctgtgttttc tttgtagaac 20
 <210> 952
 <211> 17
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 952
 ctacaactgg aggaggc 17
 <210> 953
 <211> 27
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 <400> 953
 ccaggaagca agtggaggcg tgacggu 27
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 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
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<210> 955
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 955
 gccgtcacgc ctcccttctt gatg 24
 <210> 956
 <211> 33
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 956
 ttctagacac tgaagatgtt tcagttctgt gga 33
 <210> 957
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 957
 catgcccaag aagggaggcg 20
 <210> 958
 <211> 28
 <212> DNA
 <213> Artificial Sequence
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 <400> 958
 cggaagaagc agttggaggc gtgacggc 28

<210> 959
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 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
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 <210> 960
 <211> 33
 <212> DNA
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 <223> Synthetic
 <400> 960
 ccgtcacgcc tctaattcca ttcaaaatca tct 33
 <210> 961
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 <213> Artificial Sequence
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 <223> Synthetic
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 catcctgggtg agtttgggat tcttgtaatt tata 34
 <210> 962
 <211> 25
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<213> Artificial Sequence
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 <223> Synthetic
 <400> 962
 gtaaattccag cagtaaattgc tccag 25
 <210> 963
 <211> 27
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 963
 agatgatttt gaatggaatt agaggcg 27
 <210> 964
 <211> 28
 <212> DNA
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 <223> Synthetic
 <400> 964
 cggaagaagc agttggaggc gtagcggc 28
 <210> 965
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 <212> DNA
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
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 caacgcttcc tccg 14

<210> 966
 <211> 29
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 966
 ccgccgagat cacctgtggt ttctttgta 29
 <210> 967
 <211> 32
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 967
 gtaaatccag cagtaaatgc tccagttgta ga 32
 <210> 968
 <211> 23
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 968
 gaacttgaag taggtgcact gtt 23
 <210> 969
 <211> 23
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 969
 gaacttgaag taggtgcact gtt 23

<210> 970
 <211> 23
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 970
 gaacttgaag taggtgcact gtt 23
 <210> 971
 <211> 23
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 971
 gaacttgaag taggtgcact gtt 23
 <210> 972
 <211> 23
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 972
 tacaaagaaa acacaggtga tct 23
 <210> 973
 <211> 28
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 973
 cggaggaagc agttggtgat ctcggcgg 28

<210> 974
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
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 <210> 975
 <211> 26
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 975
 aacgaggcgc acccttcttg ggcattg 26
 <210> 976
 <211> 33
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 976
 ttctagacac tgaagatgtt tcagttctgt gga 33
 <210> 977
 <211> 19
 <212> DNA

<213> Artificial Sequence
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 <223> Synthetic
 <400> 977
 catgcccaag aagggtgcg 19
 <210> 978
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 978
 cggaagaagc agttggtgcg cctcgtaa 29
 <210> 979
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 <212> DNA
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
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 caacgcttcc tccg 14
 <210> 980
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 980
 aacgaggcgc actaattcca ttcaaatca tct 33

<210> 981
 <211> 34
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 981
 catcctggtg agtttgggat tcttgtaatt tata 34
 <210> 982
 <211> 25
 <212> DNA
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 <220>
 <223> Synthetic
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 gtaaatccag cagtaaatgc tccag 25
 <210> 983
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 <220>
 <223> Synthetic
 <400> 983
 agatgatttt gaatggaatt agtggt 26
 <210> 984
 <211> 29
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 984
 cggaagaagc agttggtgcg cctcgtaa 29

<210> 985
 <211> 14
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
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 <211> 30
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 986
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 <210> 987
 <211> 22
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 987
 ccctgcagaa ggtttccttc ta 22
 <210> 988
 <211> 22
 <212> DNA

<213> Artificial Sequence
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 <223> Synthetic
 <400> 988
 ccctgcagat ggtttccttc ta 22
 <210> 989
 <211> 22
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 <213> Artificial Sequence
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 <223> Synthetic
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 ctccaagaac acaactggca gc 22
 <210> 990
 <211> 24
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 990
 ctccaagaac acaactggca gcga 24
 <210> 991
 <211> 26
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 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 991
 ctccaagaac acaactggca gcgaga 26
 <210> 992
 <211> 28
 <212> DNA

<213> Artificial Sequence
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 <223> Synthetic
 <400> 992
 cggaggaagc agttggcagc gagacagg 28
 <210> 993
 <211> 14
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 993
 caacgcttcc tccg 14
 <210> 994
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 994
 aacgaggcgc accttggagg cagcaaa 27
 <210> 995
 <211> 26
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 <223> Synthetic
 <400> 995
 aacgaggcgc accttggagg cagcaa 26

<210> 996
 <211> 24
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 <223> Synthetic
 <400> 996
 aaggtttcct tctcagttgt gtta 24
 <210> 997
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 <400> 997
 ctttgctgcc tccaaggtgc g 21
 <210> 998
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 <400> 998
 cggaggaagc agttggtgcg cctcgtaa 29
 <210> 999
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<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
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 caacgcttcc tccg 14
 <210> 1000
 <211> 29
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 1000
 cagtcacgtc tctggaggca gcaaagatg 29
 <210> 1001
 <211> 26
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 <223> Synthetic
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 aaggtttctt tctcagttgt gttcta 26
 <210> 1002
 <211> 23
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 <220>
 <223> Synthetic
 <400> 1002
 catcttttgc gcctccagag acg 23
 <210> 1003
 <211> 29

<212> DNA
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 <223> Synthetic
 <400> 1003
 gctactgaga tgaaggagac gtgactgta 29
 <210> 1004
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 <223> Synthetic
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 <223> Synthetic
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 gaattggcac tcaaattgtg tgtcagaga 29

<210> 1059
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 gttgtaaaac taaaggggag gcg 23
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 <223> Synthetic
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 cgagggttttc caaggagttg ttta 24
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<210> 1066
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25

<210> 1070

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<223> Synthetic

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agaggtacaa acgaggtttt ccaaggc

27

<210> 1071

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<400> 1072

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<210> 1073
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 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
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 <400> 1075
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<210> 1076
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 agatccctgg atcagattta gagagctc 28
 <210> 1078
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 tagctaacgg aaagaggcg 19
 <210> 1079
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 ccaggaagca agtggaggcg tgacggu 27

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 <400> 1081
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 <223> Synthetic
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 agaggtagaa acgaggtttt ccaaggaga 29
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 ctaagatccc tggatcagat ttagagag 28
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 ccaggaagca agtggaggcg tgacggu 27
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 <400> 1088
 tgcattatatt ttctgtcact ctctcttttc caatta 36
 <210> 1089
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 <212> DNA
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 <223> Synthetic
 <400> 1089
 aactcttttc ttaggcattt tgaaggtgcg 30
 <210> 1090
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 cggaggaagc agttggtgcg cctcgtaa 29

<210> 1091
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 tctgcattat ttttctgtca ctctcctctt tccaata 37
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 gaggaactgg caaaagggtg cg 22
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 gctctgcagg attttcatgt caccata 27
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 tcctccagat atccaagaag agactc 26

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 actggcaaaa ggcgggc 17
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 cggaggaaaag cagttggtgc gcctcguuua 30
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 gctctgcagg attttcatgt caccata 27
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<210> 1112
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 actggcaaaa ggcgggc 17
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 cggaggaagc agttgcggcg tgcggca 27
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 gctctgcagg attttcatgt caccata 27
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 gaactggcaa aagggtgcg 19

<210> 1119
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 ttcatacggg ttgtagttga ggtcaatg 28
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12

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<223> The residue at this position is linked to a Z28 quenching group.

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 <222> (23) .. (23)
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 <223> The modified nucleotide at this position is biotinylated deoxythymidine
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 <222> (4)..(4)
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 dye
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